WEST Search History

DATE: Monday, July 28, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR			
L3	l2 same (isolat$5 or extract$5)	29	L3
L2	(genome or DNA) with Kluyveromyces	159	L2
L1	(genome or DNA) same Kluyveromyces	2025	L1

END OF SEARCH HISTORY

STN Search History

(FILE 'HOME' ENTERED AT 15:03:54 ON 28 JUL 2003)

FILE 'MEDLINE, CAPLUS, BIOSIS, EMBASE, SCISEARCH' ENTERED AT 15:04:24 ON 28 JUL 2003

L1	16	S (FUNGUS OR KLUYVEROMYCES) AND (ENONE (A) REDUCTASE OR REDUCTA
L2	8	DUP REM L1 (8 DUPLICATES REMOVED)
L3	0	S L2 AND ENONE (A) REDUCTASE
L4	0	S ENOEN (A) REDUCTASE
L5	38	S ENONE (A) REDUCTASE
L6	12	S L5 AND (FUNGUS OR KLUYVEROMYCES OR SACCHAROMYCES)
L7	6	DUP REM L6 (6 DUPLICATES REMOVED)
L8	2	S L7 AND KLUYVEROMYCES
L9	4	S L7 NOT L8
L10	3	S L9 NOT PY>2001

L2 ANSWER 1 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:219134 BIOSIS
DN PREV200100219134
TI Peroxisomal degradation of trans-unsaturated fatty acids in the yeast Saccharomyces cerevisiae.
AU Gurvitz, Aner (1); Hamilton, Barbara; Ruis, Helmut; Hartig, Andreas
CS (1) Vienna Biocenter, Institut fuer Biochemie und Molekulare Zellbiologie, Dr Bohrgasse 9, A-1030, Vienna: AG@abc.univie.ac.at Austria
SO Journal of Biological Chemistry, (January 12, 2001) Vol. 276, No. 2, pp. 895-903. print.
ISSN: 0021-9258.
DT Article
LA English
SL English
AB Degradation of trans-unsaturated fatty acids was studied in the yeast Saccharomyces cerevisiae. Propagation of yeast cells on trans-9 elaidic acid medium resulted in transcriptional up-regulation of the SPS19 gene, whose promoter contains an oleate response element. This up-regulation depended on the Pip2p-Oaf1p transcription factor and was accompanied by induction of import-competent peroxisomes. Utilization of trans fatty acids as a single **carbon** and energy source was evaluated by monitoring the formation of clear zones around cell growth on turbid media containing fatty acids dispersed with Tween 80. For metabolizing odd-numbered trans **double bonds**, cells required the beta-oxidation auxiliary enzyme DELTA3-DELTA2-enoyl-CoA isomerase Eci1p. Metabolism of the corresponding even-numbered **double bonds** proceeded in the absence of Sps19p (2,4-dienoyl-CoA **reductase**) and Dci1p (DELTA3,5-DELTA2,4-dienoyl-CoA isomerase). trans-2,trans-4-Dienoyl-CoAs could enter beta-oxidation directly via Fox2p (2-enoyl-CoA hydratase 2 and D-specific 3-hydroxyacyl-CoA dehydrogenase) without the involvement of Sps19p, whereas trans-2,cis-4-dienoyl-CoAs could not. This **reductase**-independent metabolism of trans-2,trans-4-dienoyl-CoAs resembled the situation postulated for mammalian mitochondria in which oleic acid is degraded through a di-isomerase-dependent pathway. In this hypothetical process, trans-2,trans-4-dienoyl-CoA metabolites are generated by DELTA3-DELTA2-enoyl-CoA isomerase and DELTA3,5-DELTA2,4-dienoyl-CoA isomerase and are degraded by 2-enoyl-CoA hydratase 1 in the absence of 2,4-dienoyl-CoA **reductase**. Growth of a yeast fox2sps19DELTA mutant in which Fox2p was exchanged with rat peroxisomal multifunctional enzyme type 1 on trans-9,trans-12 linolelaidic acid medium gave credence to this theory. We propose an amendment to the current scheme of the **carbon** flux through beta-oxidation taking into account the dispensability of beta-oxidation auxiliary enzymes for metabolizing trans **double bonds** at even-numbered positions.

L2 ANSWER 2 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 2001:420342 BIOSIS
DN PREV200100420342
TI Purification and characterization of a **carbon-carbon double bond reductase** from baker's yeast.
AU Kawai, Yasushi (1); Hayashi, Motoko (1)
CS (1) Institute for Chemical Research, Kyoto University, Uji, Kyoto, 611-0011: kawai@scl.kyoto-u.ac.jp Japan
SO Journal of Molecular Catalysis B Enzymatic, (12 June, 2001) Vol. 14, No. 1-3, pp. 50. print.
Meeting Info.: 3rd Japanese Symposium on the Chemistry of Biocatalysis Atami, Shizuoka, Japan January 20-21, 2000
ISSN: 1381-1177.
DT Conference

LA English
SL English

L2 ANSWER 3 OF 8 MEDLINE on STN DUPLICATE 1
AN 2000277892 MEDLINE
DN 20277892 PubMed ID: 10817720
TI Inhibitors of sterol biosynthesis and amphotericin B reduce the viability of pneumocystis carinii f. sp. carinii.
AU Kaneshiro E S; Collins M S; Cushion M T
CS Department of Biological Sciences, University of Cincinnati, Cincinnati, Ohio 45221, USA.. Edna.Kaneshiro@uc.edu
NC RO1 AI29316 (NIAID)
RO1 AI32436 (NIAID)
RO1 AI38758 (NIAID)
+
SO ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, (2000 Jun) 44 (6) 1630-8.
Journal code: 0315061. ISSN: 0066-4804.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200007
ED Entered STN: 20000720
Last Updated on STN: 20000720
Entered Medline: 20000711
AB Pneumocystis carinii synthesizes sterols with a **double bond** at C-7 of the sterol nucleus and an alkyl group with one or two **carbons** at C-24 of the side chain. Also, some human-derived Pneumocystis carinii f. sp. hominis strains contain lanosterol derivatives with an alkyl group at C-24. These unique sterols have not been found in other pathogens of mammalian lungs. Thus, P. carinii may have important differences in its susceptibility to drugs known to block reactions in ergosterol biosynthesis in other **fungi**. In the present study, inhibitors of 3-hydroxy-3-methyglutaryl coenzyme A **reductase**, squalene synthase, squalene epoxidase, squalene epoxide-lanosterol cyclase, lanosterol demethylase, Delta(8) to Delta(7) isomerase, and S-adenosylmethionine:sterol methyltransferase were tested for their effects on P. carinii viability as determined by quantitation of cellular ATP levels in a population of organisms. Compounds within each category varied in inhibitory effect; the most effective included drugs targeted at squalene synthase, squalene epoxide-lanosterol cyclase, and Delta(8) to Delta(7) isomerase. Some drugs that are potent against ergosterol-synthesizing **fungi** had little effect against P. carinii, suggesting that substrates and/or enzymes in P. carinii sterol biosynthetic reactions are distinct. Amphotericin B is ineffective in clearing P. carinii infections at clinical doses; however, this drug apparently binds to sterols and causes permeability changes in P. carinii membranes, since it reduced cellular ATP levels in a dose-dependent fashion.

L2 ANSWER 4 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1997:460876 BIOSIS
DN PREV199799760079
TI The Saccharomyces cerevisiae peroxisomal 2,4-dienoyl-CoA **reductase** is encoded by the oleate-inducible gene SPS19.
AU Gurvitz, Aner; Rottensteiner, Hanspeter; Kilpelainen, Seppo H.; Hartig, Andreas; Hiltunen, J. Kalervo; Binder, Maximilian; Dawes, Ian W. (1); Hamilton, Barbara
CS (1) Sch. Biochemistry Molecular Genetics, Univ. New South Wales, Sydney, NSW 2052 Australia
SO Journal of Biological Chemistry, (1997) Vol. 272, No. 35, pp. 22140-22147.

ISSN: 0021-9258.
DT Article
LA English
AB beta-Oxidation is compartmentalized in mammals into both mitochondria and peroxisomes. Fatty acids with **double bonds** at even-numbered positions require for their degradation the auxiliary enzyme 2,4-dienoyl-CoA **reductase**, and at least three isoforms, two mitochondrial and one peroxisomal, exist in the rat. The Saccharomyces cerevisiae Sps19p is 34% similar to the human and rat mitochondrial **reductases**, and an SPS19 deleted strain was unable to utilize petroselineate (cis-C-18:1(6)) as the sole **carbon** source, but remained viable on oleate (cis-C-18:1(9)). Sps19p was purified to homogeneity from oleate-induced cells and the homodimeric enzyme (native molecular weight 69,000) converted 2,4-hexadienoyl-CoA into 3-hexenoyl-CoA in an NADPH-dependent manner and therefore contained 2,4-dienoyl-CoA **reductase** activity. Antibodies raised against Sps19p decorated the peroxisomal matrix of oleate-induced cells. SPS19 shares with the sporulation-specific SPS18 a common promoter region that contains an oleate response element. This element unidirectionally regulates transcription of the **reductase** and is sufficient for oleate induction of a promoterless CYC1-lacZ reporter gene. SPS19 is dispensable for growth and sporulation on solid acetate and oleate media, but is essential for these processes to occur on petroselineate.

L2 ANSWER 5 OF 8 MEDLINE on STN DUPLICATE 2
AN 96128045 MEDLINE
DN 96128045 PubMed ID: 8554504
TI Bacterial morphinone **reductase** is related to Old Yellow Enzyme.
AU French C E; Bruce N C
CS Institute of Biotechnology, University of Cambridge, U.K.
SO BIOCHEMICAL JOURNAL, (1995 Dec 15) 312 (Pt 3) 671-8.
Journal code: 2984726R. ISSN: 0264-6021.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-D21963; GENBANK-D24670; GENBANK-L06124; GENBANK-L11069; GENBANK-L25759; GENBANK-L29279; GENBANK-L33532; GENBANK-M36292; GENBANK-T04750; GENBANK-T22704; GENBANK-U37350; GENBANK-X53597; GENBANK-X67220; GENBANK-X68079
EM 199602
ED Entered STN: 19960306
Last Updated on STN: 19960306
Entered Medline: 19960220
AB Morphinone **reductase**, produced by Pseudomonas putida M10, catalyses the NADH-dependent saturation of the **carbon-carbon double bond** of morphinone and codeinone, and is believed to be involved in the metabolism of morphine and codeine. The structural gene encoding morphinone **reductase**, designated morB, was cloned from Ps. putida M10 genomic DNA by the use of degenerate oligonucleotide probes based on elements of the amino acid sequence of the purified enzyme. Sequence analysis and structural characteristics indicated that morphinone **reductase** is related to the flavoprotein alpha/beta-barrel oxidoreductases, and is particularly similar to Old Yellow Enzyme of Saccharomyces spp. and the related oestrogen-binding protein of Candida albicans. Expressed sequence tags from several plant species show high homology to these enzymes, suggesting the presence of a family of enzymes conserved in plants and **fungi**. Although related bacterial proteins are known, morphinone **reductase** appears to be more similar to the eukaryotic proteins. Morphinone **reductase** was overexpressed in Escherichia coli, and

has potential applications for the industrial preparation of semisynthetic opiates.

L2 ANSWER 6 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1992:456295 BIOSIS
DN BA94:97695
TI NADPH-DEPENDENT BETA-OXIDATION OF UNSATURATED FATTY ACIDS WITH **DOUBLE BONDS** EXTENDING FROM ODD-NUMBERED **CARBON** ATOMS.
AU SMELAND T E; NADA M; CUEBAS D; SCHULZ H
CS DEP. CHEM., CITY COLL. CITY UNIV. NEW YORK, NEW YORK, N.Y. 10031.
SO PROC NATL ACAD SCI U S A, (1992) 89 (15), 6673-6677.
CODEN: PNASA6. ISSN: 0027-8424.
FS BA; OLD
LA English
AB The mitochondrial metabolism of 5-enoyl-CoAs, which are formed during the .beta.-oxidation of unsaturated fatty acids with **double bonds** extending from odd-numbered **carbon** atoms, was studied with mitochondrial extracts and purified enzymes of .beta.-oxidation. Metabolites were identified spectrophotometrically and by high performance liquid chromatography, 5-cis-Octenoyl-CoA, a putative metabolite of linolenic acid, was efficiently dehydrogenated by medium-chain acyl-CoA dehydrogenase (EC 1.3.99.3) to 2-trans-5-cis-octadienoyl-CoA, which was isomerized to 3,5-octadienoyl-CoA either by mitochondrial .DELTA.3, .DELTA.2-enoyl-CoA isomerase (EC 5.3.3.8) or by peroxisomal trifunctional enzyme. Further isomerization of 3,5-octadienoyl-CoA to 2-trans-4-trans-octadienoyl-CoA in the presence of soluble extracts of either rat liver or rat heart mitochondria was observed and attributed to a .DELTA.3,5, .DELTA.2,4-dienoyl-CoA isomerase. Qualitatively similar results were obtained with 2-trans-5-trans-octadienoyl-CoA formed by dehydrogenation of 5-trans-octenoyl-CoA. 2-trans-4-trans-Octadienoyl-CoA was a substrate for NADPH-dependent 2,4-dienoyl-CoA **reductase** (EC 1.3.1.34). A soluble extract of rat liver mitochondria catalysed the isomerization of 2-trans-5-cis-octadienoyl-CoA to 2-trans-4-trans-octadienoyl-CoA, which upon addition of NADPH, NAD+, and CoA was chain-shortened to hexanoyl-CoA, butyryl-CoA, and acetyl-CoA. Thus we conclude that odd-numbered **double bonds**, like even-numbered **double bonds**, can be reductively removed during the .beta.-oxidation of polyunsaturated fatty acids.

L2 ANSWER 7 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1993:94551 BIOSIS
DN PREV199395049747
TI Cloning, sequencing, and disruption of the gene encoding sterol C-14 **reductase** in Saccharomyces cerevisiae.
AU Lorenz, R. Todd; Parks, Leo W. (1)
CS (1) Dep. Microbiol., North Carolina State Univ., 4515 Gardner Hall, BOx 7615, Raleigh, N.C. 27695-7615
SO DNA and Cell Biology, (1992) Vol. 11, No. 9, pp. 685-692.
ISSN: 1044-5498.
DT Article
LA English
AB A sterol C-14 **reductase** (erg24-1) mutant of Saccharomyces cerevisiae was selected in a fen1, fen2, suppressor background on the basis of nystatin resistance and ignosterol (ergosta-8,14-dienol) production. The erg24-1 alle segregated genetically as a single, recessive gene. The wild-type ERG24 gene was cloned by complementation onto a 12-kb fragment from a yeast genomic library, and subsequently subcloned onto a 2.4-kb fragment. This was sequenced and found to contain reading frame of 1,314 bp, predicting a polypeptide of 438 amino acids (M-r 50,612). A

1,088-bp internal region of the ERG24 gene was excised, replaced with a LEU2 gene, and integrated into the chromosome of the parental strain, FP13D (fen1, fen2) by gene replacement. The ERG24 null mutant produced ergosta-8,14-dienol as the major sterol, indicating that the DELTA-8-7 isomerase, DELTA-5-desaturase and the DELTA-22-desaturase were inactive on sterols with the C14 = 15 double bond.

L2 ANSWER 8 OF 8 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V. on STN
AN 90337568 EMBASE
DN 1990337568
TI Reductive biotransformations of organic compounds by cells or enzymes of yeast.
AU Ward O.P.; Young C.S.
CS Department of Biology, University of Waterloo, Waterloo, Ont., Canada
SO Enzyme and Microbial Technology, (1990) 12/7 (482-493).
ISSN: 0141-0229 CODEN: EMTED2
CY United States
DT Journal; General Review
FS 004 Microbiology
LA English
SL English
AB Saccharomyces cerevisiae catalyses the asymmetric reductive biotransformation of a variety of compounds containing a carbonyl group or **carbon-carbon double bond**.
Oxidoreductases participating in these reactions which have commercial potential in biotransformation processes are likely to have relatively broad substrate specificity. Important carbonyl **reductases** falling into this category include YADH- and yeast NADP-dependent .beta.-ketoester **reductases**. The enoyl **reductase** component of the FAS complex may have a role in asymmetric yeast reduction of **carbon-carbon double bonds** of unnatural substrates. Other nicotinamide-requiring oxidoreductases of yeast are also surveyed to rationalize observed biotransformations of whole yeast cells in terms of specific enzymes. Genetic and protein engineering may enable enzymes to be tailored to accept new substrates. A greater understanding of the enzymes and reactions involved will facilitate further optimization and exploitation of these catalytic systems in industrial processes.

L8 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2003:87072 CAPLUS
DN 138:149585
TI NADPH-dependent **enone reductase** from **Kluyveromyces** lactis and use in enzymic synthesis of saturated ketones from .alpha.,.beta.-unsatd. ketones
IN Yamamoto, Hiroaki; Kimoto, Kunihiro; Hayashi, Motoko; Kawai, Yasushi; Tokito, Nobuhiro
PA Daicel Chemical Industries, Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 21 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI JP 2003033185	A2	20030204	JP 2001-222379	20010724
PRAI JP 2001-222379		20010724		

OS CASREACT 138:149585
AB This invention provides gene and protein sequences of NADPH-dependent **enone reductase** from **Kluyveromyces** lactis, able to catalyze redn. of .alpha.,.beta.-unsatd. ketones to satd. hydrocarbons. Recombinant expression of the enzyme and use in synthesis of satd. ketones along with dehydrogenase, glucose dehydrogenase, in particular, are also claimed. The enzyme exhibits mol. wt., 92 kDa; optimum pH, 5.0-8.0, optimum temp. 37-45 .degree.C. The invention also provides detailed anal. about the substrate specificity of the enzyme. 3-Methyl-4-(3-pyridyl)-3-buten-2-one is converted to (S)-3-methyl-4-(3-pyridyl)-3-butan-2-one. Methylvinyl ketone, ethylvinyl ketone, 3-penten-2-one, methylglyoxal, 4-methyl-3-penten-2-one, 3-methyl-3-penten-2-one, 2-cyclohexenone, 3-methyl-4-(3-nitrophenyl)-3-buten-2-one were also substrates. Stereoselective synthesis of 3-pentanone from ethylvinyl ketone, (S)-3-methyl-4-(3-pyridyl)-3-butan-2-one from 3-methyl-4-(3-pyridyl)-3-buten-2-one, (S)-3-methyl-4-(3-nitrophenyl)-3-butan-2-one from 3-methyl-4-(3-nitrophenyl)-3-buten-2-one, was carried out.

L8 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2003 ACS on STN
AN 2002:660912 CAPLUS
DN 137:212850
TI Preparation of NADPH dependent **enone reductase** from **Kluyveromyces** and **Saccharomyces**
IN Yamamoto, Hiroaki; Kimoto, Kunihiro
PA Daicel Chemical Industries, Ltd., Japan
SO Jpn. Kokai Tokkyo Koho, 33 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI JP 2002247987	A2	20020903	JP 2001-49363	20010223
US 2002192782	A1	20021219	US 2002-81644	20020221
EP 1236796	A1	20020904	EP 2002-3996	20020222
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
PRAI JP 2001-49363	A	20010223		

AB This invention provides DNA and protein sequences of NADPH dependent **enone reductase** from **Kluyveromyces** lactis. The enzyme exhibits molecuar wt., 42-43 kDa; optimum pH, 6.5-7.0, optimum

temp. 37-45 .degree.C. The invention also provides detailed anal. about the substrate specificity of the enzyme. The invention also provides DNA and protein sequences of three **enone reductases** from **Saccharomyces** which share sequence homol. with its' counterpart from **Kluyveromyces**.

L10 ANSWER 1 OF 3 MEDLINE on STN
AN 1998355677 MEDLINE
DN 98355677 PubMed ID: 9692928
TI Purification and characterization of two **enone reductases** from **Saccharomyces** cerevisiae.
AU Wanner P; Tressl R
CS Technische Universitat Berlin, Institut fur Biotechnologie, Fachgebiet Chemisch-technische Analyse, Germany.
SO EUROPEAN JOURNAL OF BIOCHEMISTRY, (1998 Jul 1) 255 (1) 271-8.
Journal code: 0107600. ISSN: 0014-2956.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199808
ED Entered STN: 19980903
Last Updated on STN: 19980903
Entered Medline: 19980824
AB Two **enone reductases** catalyzing irreversibly the enantioselective reduction of alpha,beta-unsaturated carbonyls have been purified 165-fold and 257-fold, respectively, from the cytosolic fraction of **Saccharomyces** cerevisiae by means of streptomycin sulfate treatment, Sephadex G-25 filtration, DEAE-Sepharose CL-6B chromatography, blue Sepharose CL-6B chromatography and Superdex 200 preparation-grade filtration. One enzyme (E I) was NADPH-dependent, showed a molecular mass of 75 kDa and decomposed under denaturing electrophoretic conditions into two subunits of 34 kDa and 37 kDa. The other enzyme (E II) was NADH linked and the molecular mass estimated by means of Superdex 200 preparation-grade filtration, was 130 kDa. The enzyme decomposed into subunits of 56 kDa and 64 kDa on SDS/PAGE. Both enzymes were most active at pH 4.8 and accepted 1-octen-3-one, 1-hexen-3-one, 3-alken-2-ones, 4-alken-3-ones, 2-cyclohexen-1-ones, 2-alkenals, 2,4-alkadienals, 2-phenyl-2-alkenals, and 2-alkyl-2-alkenals as substrates. Both enzymes showed their highest activities with 1-hexen-3-one and 1-octen-3-one, respectively. The Km values for 1-octen-3-one were estimated as 0.54 mM (E I) and 0.20 mM (E II), respectively. Both enzymes catalyzed the enantioselective reduction of cis- and trans-2-phenyl-2-butenal into (R)-2-phenylbutanal.

L10 ANSWER 2 OF 3 CAPLUS COPYRIGHT 2003 ACS on STN
AN 1987:594506 CAPLUS
DN 107:194506
TI Inducibility of an **enone reductase** system in the **fungus** Beauveria sulfurescens: application in enantioselective organic synthesis
AU Fauve, Annie; Renard, Michel F.; Veschambre, Henri
CS Lab. Chim. Org. Biol., Univ. Clermont-II, Aubiere, 63170, Fr.
SO Journal of Organic Chemistry (1987), 52(22), 4893-7
CODEN: JOCEAH; ISSN: 0022-3263
DT Journal
LA English
AB Microbiol. redn. of .alpha.,.beta.-unsatd. carbonyl compds. is studied. Inducibility of the **enone reductase** system of B. sulfurescens is reported. The best inducer is cyclohex-2-en-1-one. An appropriate procedure using induced resting mycelium is developed to reduce substituted cyclohexenones that are shown to be unable to induce the reducing enzyme. Optically pure trans-(2R,6R)-(-)-2,6-dimethylcyclohexan-1-one and trans-(2R,6R)-(-)-2,6-dimethyl-cyclohexan-1-ol are obtained from (.+-.)-2.6-dimethylcyclohex-2-en-1-one along with optically pure (6S)-(-)-2,6-dimethylcyclohex-2-en-1-one.

L10 ANSWER 3 OF 3 SCISEARCH COPYRIGHT 2003 THOMSON ISI on STN
AN 87:626619 SCISEARCH
GA The Genuine Article (R) Number: K7137
TI INDUCIBILITY OF AN **ENONE REDUCTASE** SYSTEM IN THE **FUNGUS** BEAUVERIA-SULFURESCENS - APPLICATION IN ENANTIOSELECTIVE ORGANIC-SYNTHESIS
AU FAUVE A; RENARD M F; VESCHAMBRE H (Reprint)
CS UNIV CLERMONT FERRAND 2, CHIM ORGAN BIOL LAB, CNRS, UA 485, F-63170 AUBIERE, FRANCE
CYA FRANCE
SO JOURNAL OF ORGANIC CHEMISTRY, (1987) Vol. 52, No. 22, pp. 4893-4897.
DT Article; Journal
FS PHYS; LIFE
LA ENGLISH
REC Reference Count: 15

Generate Collection

L3: Entry 10 of 29 File: USPT Feb 5, 2002

DOCUMENT-IDENTIFIER: US 6344341 B1
TITLE: Increased production of secreted proteins by recombinant yeast cells

Detailed Description Text (75):
Genomic .DNA from the fungal species Saccharomyces cerevisiae, Schizosaccharomyces pombe, Kluyveromyces lactis, Pichia pastoris, Pichia stipitis, Candida utilis, and Yarrowia lipolytica were isolated, digested with the HindIII restriction enzyme, separated electrophoretically in an 0.8% agarose gel and blotted on a nylon filter. Southern hybridization of the filter was carried out at different stringencies using the Saccharomyces SEB1 gene coding region as a probe. Hybridization in a mixture containing 30% formamide, 6.times.SSC, 10.times.Denhardt's, 0.5% SDS, 100 mg/ml herring sperm DNA and 10 mg/ml polyA at 35.degree. C. and washing 15 minutes in 6.times.SSC, 0.1% SDS at 42.degree. C. and 2.times.30 minutes in 2.times.SSC, 0.1% SDS at 42.degree. C. revealed clear hybridizing bands in DNA derived from S. cerevisiae, S. pombe, K. lactis, P. stipitis and Y. lipolytica, and a much weaker band in DNA of C. utilis (FIG. 7).

DOCUMENT-IDENTIFIER: US 4943529 A
**** See image for Certificate of Correction ****
TITLE: Kluyveromyces as a host strain

Detailed Description Text (119):
Chromosomal DNA was isolated from Kluyveromyces lactis strain CBS 2360 (Das and Hollenberg, Current Genetics (1982) 5:123-128), cleaved with XhoI, and separated according to size on a sucrose gradient. Fractions containing the lactase gene were detected with a LAC4 probe from plasmid pK16 (see Example 16.C2) after spotting the DNA on a nitrocellulose filter. DNA containing the LAC4 gene was cloned into the XhoI site of plasmid pPA153-215 (Andreoli, Mol. Gen. Gen (1985) 199:372-380) giving rise to plasmid pPA31. An XbaI fragment of pPA31 containing the lactase gene was subcloned in the XbaI site of pUC19 (Yanisch-Perron et al., Gene (1985) 33:103-119) which yields plasmid pUCla56.